

SEQUENCE LISTING

<110> APPLICANT: Novartis AG
 <120> TITLE OF INVENTION: Organic Compound
 <130> FILE REFERENCE: 4-32761P1/UNZ
 <140> CURRENT APPLICATION NUMBER: US/10/538,201
 <141> CURRENT FILING DATE: 2006-03-08
 <160> NUMBER OF SEQ ID NOS: 48
 <170> SOFTWARE: PatentIn version 3.1

<210> SEQ ID NO 1
 <211> LENGTH: 18
 <212> TYPE: PRT
 <213> ORGANISM: Rattus norvegicus
 <220> FEATURE:
 <221> NAME/KEY: PEPTIDE
 <222> LOCATION: (1)..(18)
 <223> OTHER INFORMATION: rat NogoA_623-640
 <400> SEQUENCE: 1
 Ser Tyr Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu
 1 5 10 15
 Glu Ala

<210> SEQ ID NO 2
 <211> LENGTH: 221
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: CHAIN
 <222> LOCATION: (1)..(221)
 <223> OTHER INFORMATION: Variable part of Heavy Chain of 11C7 with leader sequence
 <400> SEQUENCE: 2
 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
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 Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
 20 25 30
 Gly Gly Ser Leu Lys Leu Ser Cys Val Val Ser Gly Phe Asp Phe Arg
 35 40 45
 Arg Asn Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 50 55 60
 Trp Ile Gly Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro
 65 70 75 80
 Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
 85 90 95
 Leu Tyr Leu Gln Val Ser Thr Val Arg Ser Glu Asp Thr Ala Leu Tyr
 100 105 110
 Tyr Cys Val Arg Pro Val Trp Met Tyr Ala Met Asp Tyr Trp Gly Gln
 115 120 125
 Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
 130 135 140
 Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
 145 150 155 160
 Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
 165 170 175
 Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
 180 185 190
 Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
 195 200 205
 Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
 210 215 220

<210> SEQ ID NO 3
 <211> LENGTH: 238
 <212> TYPE: PRT

<213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: CHAIN
 <222> LOCATION: (1)..(238)
 <223> OTHER INFORMATION: Light Chain of 11C7 with leader sequence
 <400> SEQUENCE: 3

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Thr	Ser	Gly	Asp	Val	Leu	Leu	Thr	Gln	Thr	Pro	Leu	Thr	Leu	Ser	Ile
			20					25					30		
Thr	Ile	Gly	Gln	Pro	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	Gln	Ser	Leu
		35					40					45			
Leu	His	Ser	Asp	Gly	Lys	Thr	Tyr	Leu	Asn	Trp	Leu	Leu	Gln	Arg	Pro
	50					55					60				
Gly	Gln	Ser	Pro	Lys	Arg	Leu	Ile	Tyr	Leu	Val	Ser	Lys	Leu	Asp	Ser
65					70					75				80	
Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr
				85					90					95	
Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Leu	Tyr	Tyr	Cys
			100					105					110		
Trp	Gln	Gly	Thr	His	Phe	Pro	Gln	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu
		115					120					125			
Glu	Ile	Lys	Arg	Ala	Asp	Ala	Ala	Pro	Thr	Val	Ser	Ile	Phe	Pro	Pro
	130					135					140				
Ser	Ser	Glu	Gln	Leu	Thr	Ser	Gly	Gly	Ala	Ser	Val	Val	Cys	Phe	Leu
145					150					155					160
Asn	Asn	Phe	Tyr	Pro	Lys	Asp	Ile	Asn	Val	Lys	Trp	Lys	Ile	Asp	Gly
				165					170					175	
Ser	Glu	Arg	Gln	Asn	Gly	Val	Leu	Asn	Ser	Trp	Thr	Asp	Gln	Asp	Ser
			180					185					190		
Lys	Asp	Ser	Thr	Tyr	Ser	Met	Ser	Ser	Thr	Leu	Thr	Leu	Thr	Lys	Asp
		195				200						205			
Glu	Tyr	Glu	Arg	His	Asn	Ser	Tyr	Thr	Cys	Glu	Ala	Thr	His	Lys	Thr
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<210> SEQ ID NO 4
 <211> LENGTH: 3919
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(3579)
 <223> OTHER INFORMATION: Human NogoA
 <400> SEQUENCE: 4

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1				5					10					15		
ccc	cgg	ccg	cag	ccc	gcg	ttc	aag	tac	cag	ttc	gtg	agg	gag	ccc	gag	96
Pro	Arg	Pro	Gln	Pro	Ala	Phe	Lys	Tyr	Gln	Phe	Val	Arg	Glu	Pro	Glu	
			20					25					30			
gac	gag	gag	gaa	gaa	gag	gag	gag	gaa	gag	gag	gac	gag	gac	gaa	gac	144
Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Asp	Glu	Asp	
		35					40				45					
ctg	gag	gag	ctg	gag	gtg	ctg	gag	agg	aag	ccc	gcc	gcc	ggg	ctg	tcc	192
Leu	Glu	Glu	Leu	Glu	Val	Leu	Glu	Arg	Lys	Pro	Ala	Ala	Gly	Leu	Ser	
	50					55					60					
gcg	gcc	cca	gtg	ccc	acc	gcc	cct	gcc	gcc	ggc	gcg	ccc	ctg	atg	gac	240
Ala	Ala	Pro	Val	Pro	Thr	Ala	Pro	Ala	Ala	Gly	Ala	Pro	Leu	Met	Asp	
65					70					75				80		
ttc	gga	aat	gac	ttc	gtg	ccg	ccg	gcg	ccc	gga	ccc	ctg	ccg	gcc		288
Phe	Gly	Asn	Asp	Phe	Val	Pro	Pro	Ala	Pro	Arg	Gly	Pro	Leu	Pro	Ala	
				85					90					95		

gct Ala	ccc Pro	ccc Pro	gtc Val 100	gcc Ala	ccg Pro	gag Glu	cgg Arg	cag Gln 105	ccg Pro	tct Ser	tgg Trp	gac Asp	ccg Pro 110	agc Ser	ccg Pro	336
gtg Val	tcg Ser	tcg Ser 115	acc Thr	gtg Val	ccc Pro	gcg Ala	cca Pro 120	tcc Ser	ccg Pro	ctg Leu	tct Ser	gct Ala 125	gcc Ala	gca Ala	gtc Val	384
tcg Ser	ccc Pro 130	tcc Ser	aag Lys	ctc Leu	cct Pro	gag Glu 135	gac Asp	gac Asp	gag Glu	cct Pro	ccg Pro 140	gcc Ala	cgg Arg	cct Pro	ccc Pro	432
cct Pro 145	cct Pro	ccc Pro	ccg Pro	gcc Ala	agc Ser 150	gtg Val	agc Ser	ccc Pro	cag Gln 155	gca Ala	gag Glu	ccc Pro	gtg Val	tgg Trp 160	acc Thr 160	480
ccg Pro	cca Pro	gcc Ala	ccg Pro	gct Ala 165	ccc Pro	gcc Ala	gcg Ala	ccc Pro	ccc Pro 170	tcc Ser	acc Thr	ccg Pro	gcc Ala	gcg Ala 175	ccc Pro	528
aag Lys	cgc Arg	agg Arg	ggc Gly 180	tct Ser	tcg Ser	ggc Gly	tca Ser	gtg Val 185	gat Asp	gag Glu	acc Thr	ctt Leu	ttt Phe 190	gct Ala	ctt Leu	576
cct Pro	gct Ala 195	gca Ala	tct Ser	gag Glu	cct Pro	gtg Val	ata Ile 200	cgc Arg	tcc Ser	tct Ser	gca Ala	gaa Glu 205	aat Asn	atg Met	gac Asp	624
ttg Leu	aag Lys 210	gag Glu	cag Gln	cca Pro	ggg Gly	aac Asn 215	act Thr	att Ile	tcg Ser	gct Ala	ggg Gly 220	caa Gln	gag Glu	gat Asp	ttc Phe	672
cca Pro 225	tct Ser	gtc Val	ctg Leu	ctt Leu	gaa Glu 230	act Thr	gct Ala	gct Ala	tct Ser	ctt Leu 235	cct Pro	tct Ser	ctg Leu	tct Ser	cct Pro 240	720
ctc Leu	tca Ser	gcc Ala	gct Ala	tct Ser 245	ttc Phe	aaa Lys	gaa Glu	cat His	gaa Glu 250	tac Tyr	ctt Leu	ggg Gly	aat Asn	ttg Leu 255	tca Ser	768
aca Thr	gta Val	tta Leu	ccc Pro 260	act Thr	gaa Glu	gga Gly	aca Thr	ctt Leu 265	caa Gln	gaa Glu	aat Asn	gtc Val 270	agt Ser	gaa Glu	gct Ala	816
tct Ser	aaa Lys	gag Glu 275	gtc Val	tca Ser	gag Glu	aag Lys	gca Ala 280	act Lys	cta Thr	ctc Leu	ata Ile 285	gat Asp	aga Arg	gat Asp		864
tta Leu	aca Thr 290	gag Glu	ttt Phe	tca Ser	gaa Glu	tta Leu 295	gaa Glu	tac Tyr	tca Ser	gaa Glu	atg Met 300	gga Gly	tca Ser	tcg Ser	ttc Phe	912
agt Ser 305	gtc Val	tct Ser	cca Pro	aaa Lys	gca Ala 310	tct Glu	gcc Ala	gta Val	ata Ile 315	gta Val	gca Ala	aat Asn	cct Pro	agg Arg 320		960
gaa Glu	gaa Glu	ata Ile	atc Ile	gtg Val 325	aaa Lys	aat Asn	aaa Lys	gat Asp	gaa Glu 330	gaa Glu	gag Glu	aag Lys	tta Leu	gtt Val 335	agt Ser	1008
aat Asn	aac Asn	atc Ile	ctt Leu 340	cat His	aat Asn	caa Gln	caa Gln	gag Glu 345	tta Leu	cct Pro	aca Thr	gct Ala	ctt Leu 350	act Thr	aaa Lys	1056
ttg Leu	gtt Val	aaa Lys 355	gag Glu	gat Asp	gaa Glu	gtt Val	gtg Val 360	tct Ser	tca Ser	gaa Glu	aaa Lys	gca Ala 365	aaa Lys	gac Asp	agt Ser	1104
ttt Phe	aat Asn 370	gaa Glu	aag Lys	aga Arg	gtt Val	gca Ala 375	gtg Val	gaa Glu	gct Ala	cct Pro	atg Met 380	agg Arg	gag Glu	gaa Glu	tat Tyr	1152
gca Ala 385	gac Asp	ttc Phe	aaa Lys	cca Pro	ttt Phe 390	gag Glu	cga Arg	gta Val	tgg Trp	gaa Glu 395	gtg Val	aaa Lys	gat Asp	agt Ser	aag Lys 400	1200
gaa Glu	gat Asp	agt Ser	gat Asp	atg Met 405	ttg Leu	gct Ala	gct Ala	gga Gly	ggg Gly 410	aaa Lys	atc Ile	gag Glu	agc Ser	aac Asn 415	ttg Leu	1248
gaa Glu	agt Ser	aaa Lys	gtg Val 420	gat Asp	aaa Lys	aaa Lys	tgt Cys	ttt Phe 425	gca Ala	gat Asp	agc Ser	ctt Leu	gag Glu 430	caa Gln	act Thr	1296
aat Asn	cac His	gaa Glu	aaa Lys	gat Asp	agt Ser	gag Glu	agt Ser	agt Ser	aat Asn	gat Asp	gat Asp	act Thr	tct Ser	ttc Phe	ccc Pro	1344

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agt	acg	cca	gaa	ggc	ata	aag	gat	cgt	tca	gga	gca	tat	atc	aca	tgt		1392
Ser	Thr	Pro	Glu	Gly	Ile	Lys	Asp	Arg	Ser	Gly	Ala	Tyr	Ile	Thr	Cys		
	450					455					460						
gct	ccc	ttt	aac	cca	gca	gca	act	gag	agc	att	gca	aca	aac	att	ttt		1440
Ala	Pro	Phe	Asn	Pro	Ala	Ala	Thr	Glu	Ser	Ile	Ala	Thr	Asn	Ile	Phe		
	465				470					475					480		
cct	ttg	tta	gga	gat	cct	act	tca	gaa	aat	aag	acc	gat	gaa	aaa	aaa		1488
Pro	Leu	Leu	Gly	Asp	Pro	Thr	Ser	Glu	Asn	Lys	Thr	Asp	Glu	Lys	Lys		
				485					490					495			
ata	gaa	gaa	aag	aag	gcc	caa	ata	gta	aca	gag	aag	aat	act	agc	acc		1536
Ile	Glu	Glu	Lys	Lys	Ala	Gln	Ile	Val	Thr	Glu	Lys	Asn	Thr	Ser	Thr		
			500					505					510				
aaa	aca	tca	aac	cct	ttt	ctt	gta	gca	gca	cag	gat	tct	gag	aca	gat		1584
Lys	Thr	Ser	Asn	Pro	Phe	Leu	Val	Ala	Ala	Gln	Asp	Ser	Glu	Thr	Asp		
			515				520					525					
tat	gtc	aca	aca	gat	aat	tta	aca	aag	gtg	act	gag	gaa	gtc	gtg	gca		1632
Tyr	Val	Thr	Thr	Asp	Asn	Leu	Thr	Lys	Val	Thr	Glu	Glu	Val	Val	Ala		
	530					535					540						
aac	atg	cct	gaa	ggc	ctg	act	cca	gat	tta	gta	cag	gaa	gca	tgt	gaa		1680
Asn	Met	Pro	Glu	Gly	Leu	Thr	Pro	Asp	Leu	Val	Gln	Glu	Ala	Cys	Glu		
	545				550					555					560		
agt	gaa	ttg	aat	gaa	gtt	act	ggc	aca	aag	att	gct	tat	gaa	aca	aaa		1728
Ser	Glu	Leu	Asn	Glu	Val	Thr	Gly	Thr	Lys	Ile	Ala	Tyr	Glu	Thr	Lys		
				565					570					575			
atg	gac	ttg	gtt	caa	aca	tca	gaa	gtt	atg	caa	gag	tca	ctc	tat	cct		1776
Met	Asp	Leu	Val	Gln	Thr	Ser	Glu	Val	Met	Gln	Glu	Ser	Leu	Tyr	Pro		
			580					585					590				
gca	gca	cag	ctt	tgc	cca	tca	ttt	gaa	gag	tca	gaa	gct	act	cct	tca		1824
Ala	Ala	Gln	Leu	Cys	Pro	Ser	Phe	Glu	Glu	Ser	Glu	Ala	Thr	Pro	Ser		
		595					600					605					
cca	gtt	ttg	cct	gac	att	gtt	atg	gaa	gca	cca	ttg	aat	tct	gca	gtt		1872
Pro	Val	Leu	Pro	Asp	Ile	Val	Met	Glu	Ala	Pro	Leu	Asn	Ser	Ala	Val		
	610					615					620						
cct	agt	gct	ggc	gct	tcc	gtg	ata	cag	ccc	agc	tca	tca	cca	tta	gaa		1920
Pro	Ser	Ala	Gly	Ala	Ser	Val	Ile	Gln	Pro	Ser	Ser	Ser	Pro	Leu	Glu		
	625				630				635					640			
gct	tct	tca	gtt	aat	tat	gaa	agc	ata	aaa	cat	gag	cct	gaa	aac	ccc		1968
Ala	Ser	Ser	Val	Asn	Tyr	Glu	Ser	Ile	Lys	His	Glu	Pro	Glu	Asn	Pro		
				645					650					655			
cca	cca	tat	gaa	gag	gcc	atg	agt	gta	tca	cta	aaa	aaa	gta	tca	gga		2016
Pro	Pro	Tyr	Glu	Glu	Ala	Met	Ser	Val	Ser	Leu	Lys	Lys	Val	Ser	Gly		
			660					665					670				
ata	aag	gaa	gaa	att	aaa	gag	cct	gaa	aat	att	aat	gca	gct	ctt	caa		2064
Ile	Lys	Glu	Glu	Ile	Lys	Glu	Pro	Glu	Asn	Ile	Asn	Ala	Ala	Leu	Gln		
		675					680					685					
gaa	aca	gaa	gct	cct	tat	ata	tct	att	gca	tgt	gat	tta	att	aaa	gaa		2112
Glu	Thr	Glu	Ala	Pro	Tyr	Ile	Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu		
	690					695				700							
aca	aag	ctt	tct	gct	gaa	cca	gct	ccg	gat	ttc	tct	gat	tat	tca	gaa		2160
Thr	Lys	Leu	Ser	Ala	Glu	Pro	Ala	Pro	Asp	Phe	Ser	Asp	Tyr	Ser	Glu		
	705			710						715				720			
atg	gca	aaa	gtt	gaa	cag	cca	gtg	cct	gat	cat	tct	gag	cta	gtt	gaa		2208
Met	Ala	Lys	Val	Glu	Gln	Pro	Val	Pro	Asp	His	Ser	Glu	Leu	Val	Glu		
				725				730					735				
gat	tcc	tca	cct	gat	tct	gaa	cca	gtt	gac	tta	ttt	agt	gat	gat	tca		2256
Asp	Ser	Ser	Pro	Asp	Ser	Glu	Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp	Ser		
			740					745					750				
ata	cct	gac	gtt	cca	caa	aaa	caa	gat	gaa	act	gtg	atg	ctt	gtg	aaa		2304
Ile	Pro	Asp	Val	Pro	Gln	Lys	Gln	Asp	Glu	Thr	Val	Met	Leu	Val	Lys		
		755				760					765						
gaa	agt	ctc	act	gag	act	tca	ttt	gag	tca	atg	ata	gaa	tat	gaa	aat		2352
Glu	Ser	Leu	Thr	Glu	Thr	Ser	Phe	Glu	Ser	Met	Ile	Glu	Tyr	Glu	Asn		
	770					775					780						
aag	gaa	aaa	ctc	agt	gct	ttg	cca	cct	gag	gga	gga	aag	cca	tat	ttg		2400

Lys 785	Glu	Lys	Leu	Ser	Ala 790	Leu	Pro	Pro	Glu	Gly 795	Gly	Lys	Pro	Tyr	Leu 800	
gaa Glu	tct Ser	ttt Phe	aag Lys	ctc Leu	agt Ser	tta Leu	gat Asp	aac Asn	aca Thr	aaa Lys	gat Asp	acc Thr	ctg Leu	tta Leu	cct Pro	2448
gat Asp	gaa Glu	gtt Val	tca Ser	aca Thr	ttg Leu	agc Ser	aaa Lys	aag Lys	gag Glu	aaa Lys	att Ile	cct Pro	ttg Leu	cag Gln	atg Met	2496
gag Glu	gag Glu	ctc Leu	agt Ser	act Thr	gca Ala	gtt Val	tat Tyr	tca Ser	aat Asn	gat Asp	gac Asp	tta Leu	ttt Phe	att Ile	tct Ser	2544
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att Ile	gaa Glu	att Ile	ata Ile	gat Asp	gag Glu	ttc Phe	cct Pro	aca Thr	ttg Leu	atc Ile	agt Ser	tct Ser	aaa Lys	act Thr	gat Asp	2640
tca Ser	ttt Phe	tct Ser	aaa Lys	tta Leu	gcc Ala	agg Arg	gaa Glu	tat Tyr	act Thr	gac Asp	cta Leu	gaa Glu	gta Val	tcc Ser	cac His	2688
aaa Lys	agt Ser	gaa Glu	att Ile	gct Ala	aat Asn	gcc Ala	ccg Pro	gat Asp	gga Gly	gct Ala	ggg Gly	tca Ser	ttg Leu	cct Pro	tg Cys	2736
aca Thr	gaa Glu	ttg Leu	ccc Pro	cat His	gac Asp	ctt Leu	tct Ser	ttg Leu	aag Lys	aac Asn	ata Ile	caa Gln	ccc Pro	aaa Lys	gtt Val	2784
gaa Glu	gag Glu	aaa Lys	atc Ile	agt Ser	ttc Phe	tca Ser	gat Asp	gac Asp	ttt Phe	tct Ser	aaa Lys	aat Asn	ggg Gly	tct Ser	gct Ala	2832
aca Thr	tca Ser	aag Lys	gtg Val	ctc Leu	tta Leu	ttg Leu	cct Pro	cca Pro	gat Asp	gtt Val	tct Ser	gct Ala	ttg Leu	gcc Ala	act Thr	2880
caa Gln	gca Ala	gag Glu	ata Ile	gag Glu	agc Ser	ata Ile	gtt Val	aaa Lys	ccc Pro	aaa Lys	gtt Val	ctt Leu	gtg Val	aaa Lys	gaa Glu	2928
gct Ala	gag Glu	aaa Lys	aaa Lys	ctt Leu	cct Pro	tcc Ser	gat Asp	aca Thr	gaa Glu	aaa Lys	gag Glu	gac Asp	aga Arg	tca Ser	cca Pro	2976
tct Ser	gct Ala	ata Ile	ttt Phe	tca Ser	gca Ala	gag Glu	ctg Leu	agt Ser	aaa Lys	act Thr	tca Ser	gtt Val	gtt Val	gac Asp	ctc Leu	3024
ctg Leu	tac Tyr	tg Trp	aga Arg	gac Asp	att Ile	aag Lys	aag Lys	act Thr	gga Gly	gtg Val	gtg Val	ttt Phe	ggt Gly	gcc Ala		3069
agc Ser	cta Leu	ttc Phe	ctg Leu	ctg Leu	ctt Leu	tca Ser	ttg Leu	aca Thr	gta Val	ttc Phe	agc Ser	att Ile	gtg Val	agc Ser		3114
gta Val	aca Thr	gcc Ala	tac Tyr	att Ile	gcc Ala	ttg Leu	gcc Ala	ctg Leu	ctc Leu	tct Ser	gtg Val	acc Thr	atc Ile	agc Ser		3159
ttt Phe	agg Arg	ata Ile	tac Tyr	aag Lys	ggt Gly	gtg Val	atc Ile	caa Gln	gct Ala	atc Ile	cag Gln	aaa Lys	tca Ser	gat Asp		3204
gaa Glu	ggc Gly	cac His	cca Pro	ttc Phe	agg Arg	gca Ala	tat Tyr	ctg Leu	gaa Glu	tct Ser	gaa Glu	gtt Val	gct Ala	ata Ile		3249
tct Ser	gag Glu	gag Glu	ttg Leu	gtt Val	cag Gln	aag Lys	tac Tyr	agt Ser	aat Asn	tct Ser	gct Ala	ctt Leu	ggt Gly	cat His		3294
gtg Val	aac Asn	tg Cys	acg Thr	ata Ile	aag Lys	gaa Glu	ctc Leu	agg Arg	cgc Arg	ctc Leu	ttc Phe	tta Leu	gtt Val	gat Asp		3339
gat Asp	tta Leu	gtt Val	gat Asp	tct Ser	ctg Leu	aag Lys	ttt Phe	gca Ala	gtg Val	ttg Leu	atg Met	tg Trp	gta Val	ttt Phe		3384

acc tat gtt ggt gcc ttg ttt aat ggt ctg aca cta ctg att ttg	3429
Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu	
1130 1135 1140	
gct ctc att tca ctc ttc agt gtt cct gtt att tat gaa cgg cat	3474
Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His	
1145 1150 1155	
cag gca cag ata gat cat tat cta gga ctt gca aat aag aat gtt	3519
Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val	
1160 1165 1170	
aaa gat gct atg gct aaa atc caa gca aaa atc cct gga ttg aag	3564
Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys	
1175 1180 1185	
cgc aaa gct gaa tga aaacgccc aaataattagt aggagttcat ctttaaaggg	3619
Arg Lys Ala Glu	
1190	
gatattcatt tgattatacg ggggagggtc agggaagaac gaaccttgac gttgcagtgc	3679
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acctgtcttg actgccatgt gttcatcatc ttaagtattg taagctgcta tgtatggatt	3799
taaaccgtaa tcatatcttt ttcctatctg aggcactggg ggaataaaaa acctgtatat	3859
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<210> SEQ ID NO 5

<211> LENGTH: 1192

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 5

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Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp	
35 40 45	
Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser	
50 55 60	
Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp	
65 70 75 80	
Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala	
85 90 95	
Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro	
100 105 110	
Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val	
115 120 125	
Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro	
130 135 140	
Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr	
145 150 155 160	
Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro	
165 170 175	
Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu	
180 185 190	
Pro Ala Ala Ser Glu Pro Val Ile Arg Ser Ser Ala Glu Asn Met Asp	
195 200 205	
Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe	
210 215 220	
Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro	
225 230 235 240	
Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Gly Asn Leu Ser	
245 250 255	
Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala	
260 265 270	
Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile Asp Arg Asp	
275 280 285	
Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe	
290 295 300	
Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn Pro Arg	

305	Glu	Glu	Ile	Ile	Val	310	Lys	Asn	Lys	Asp	Glu	315	Glu	Glu	Lys	Leu	Val	320	Ser
	Asn	Asn	Ile	Leu	325	His	Asn	Gln	Gln	Glu	330	Leu	Pro	Thr	Ala	Leu	335	Thr	Lys
	Leu	Val	Lys	Glu	340	Asp	Glu	Val	Val	Ser	345	Ser	Glu	Lys	Ala	Lys	350	Asp	Ser
	Phe	Asn	Glu	Lys	355	Arg	Val	Ala	Val	Glu	360	Ala	Pro	Met	Arg	Glu	365	Glu	Tyr
	Ala	Asp	Phe	Lys	370	Pro	Phe	Glu	Arg	Val	375	Trp	Glu	Val	Lys	Asp	380	Ser	Lys
	385	Glu	Asp	Ser	Asp	Met	Leu	Ala	Ala	Gly	390	Gly	Lys	Ile	Glu	Ser	400	Asn	Leu
					405						410	Ala	Asp	Ser	Leu	Glu	415	Gln	Thr
	Asn	His	Glu	Lys	420	Asp	Ser	Glu	Ser	425	Asn	Asp	Asp	Thr	430	Ser	435	Phe	Pro
	Ser	Thr	Pro	Glu	Gly	Ile	Lys	Asp	Arg	Ser	440	Gly	Ala	Tyr	Ile	Thr	445	Cys	
	Ala	Pro	Phe	Asn	Pro	Ala	Ala	Thr	Glu	Ser	450	Ile	Ala	Thr	Asn	Ile	455	Phe	
	465	Pro	Leu	Leu	Gly	Asp	Pro	Thr	Ser	Glu	460	Asn	Lys	Thr	Asp	Glu	465	Lys	Lys
					485						490	Thr	Glu	Lys	Asn	Thr	495	Ser	Thr
	Ile	Glu	Glu	Lys	Lys	Ala	Gln	Ile	Val	500	Thr	Glu	Lys	Asn	Thr	505	510	Ser	Thr
	Lys	Thr	Ser	Asn	Pro	Phe	Leu	Val	Ala	Ala	Gln	Asp	Ser	515	Glu	Thr	520	Asp	
	Tyr	Val	Thr	Thr	Asp	Asn	Leu	Thr	Lys	Val	525	Thr	Glu	Val	Val	Ala	530		
	Asn	Met	Pro	Glu	Gly	Leu	Thr	Pro	Asp	Leu	535	Val	Gln	Glu	Ala	Cys	540	Glu	
	545	Ser	Glu	Leu	Asn	Glu	Val	Thr	Gly	Thr	550	Lys	Ile	Ala	Tyr	Glu	555	Thr	Lys
	Met	Asp	Leu	Val	Gln	Thr	Ser	Glu	Val	565	Met	Gln	Glu	Ser	Leu	Tyr	570	Pro	
	Ala	Ala	Gln	Leu	Cys	Pro	Ser	Phe	Glu	Glu	580	Ser	Glu	Ala	Thr	Pro	585	Ser	
	Pro	Val	Leu	Pro	Asp	Ile	Val	Met	Glu	Ala	595	Pro	Leu	Asn	Ser	Ala	600	Val	
	Pro	Ser	Ala	Gly	Ala	Ser	Val	Ile	Gln	Pro	605	Ser	Ser	Pro	Leu	Glu	610		
	625	Ala	Ser	Ser	Val	Asn	Tyr	Glu	Ser	Ile	615	Lys	His	Glu	Pro	Glu	620	Asn	Pro
	Pro	Pro	Tyr	Glu	Ala	Met	Ser	Val	Ser	Leu	630	Ser	Leu	Lys	Lys	Val	635	Ser	Gly
	Ile	Lys	Glu	Glu	Ile	Lys	Glu	Pro	Glu	Asn	645	Ile	Asn	Ala	Ala	Leu	650	Gln	
	Glu	Thr	Glu	Ala	Pro	Tyr	Ile	Ser	Ile	Ala	660	Cys	Asp	Leu	Ile	Lys	665	Glu	
	Thr	Lys	Leu	Ser	Ala	Glu	Pro	Ala	Pro	Asp	675	Phe	Ser	Asp	Tyr	Ser	680	Glu	
	705	Met	Ala	Lys	Val	Glu	Gln	Pro	Val	Pro	695	His	Ser	Glu	Leu	Val	700	Glu	
	Asp	Ser	Ser	Pro	Asp	Ser	Glu	Pro	Val	Asp	710	Leu	Phe	Ser	Asp	Asp	715	Ser	
	Ile	Pro	Asp	Val	Pro	Gln	Lys	Gln	Asp	Glu	725	Thr	Val	Met	Leu	Val	730	Lys	
	Glu	Ser	Leu	Thr	Glu	Thr	Ser	Phe	Glu	Ser	740	Met	Ile	Glu	Tyr	Glu	745	Asn	
	Lys	Glu	Lys	Leu	Ser	Ala	Leu	Pro	Pro	Glu	755	Gly	Gly	Lys	Pro	Tyr	760	Leu	
	785	Glu	Ser	Phe	Lys	Leu	Ser	Leu	Asp	Asn	775	Lys	Asp	Thr	Leu	Leu	780	Pro	
	Asp	Glu	Val	Ser	Thr	Leu	Ser	Lys	Lys	Glu	790	Ile	Pro	Leu	Gln	Met	800		
				820							825						830		

Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser
 835 840 845
 Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro
 850 855 860
 Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp
 865 870 875 880
 Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His
 885 890 895
 Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys
 900 905 910
 Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val
 915 920 925
 Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala
 930 935 940
 Thr Ser Lys Val Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr
 945 950 955 960
 Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu
 965 970 975
 Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro
 980 985 990
 Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu
 995 1000 1005
 Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala
 1010 1015 1020
 Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser
 1025 1030 1035
 Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser
 1040 1045 1050
 Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp
 1055 1060 1065
 Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile
 1070 1075 1080
 Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His
 1085 1090 1095
 Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp
 1100 1105 1110
 Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe
 1115 1120 1125
 Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu
 1130 1135 1140
 Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His
 1145 1150 1155
 Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val
 1160 1165 1170
 Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys
 1175 1180 1185
 Arg Lys Ala Glu
 1190

<210> SEQ ID NO 6

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: PEPTIDE

<222> LOCATION: (1)..(18)

<223> OTHER INFORMATION: Human NogoA_623-640

<400> SEQUENCE: 6

Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu
 1 5 10 15
 Glu Ala

<210> SEQ ID NO 7

<211> LENGTH: 819

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: PEPTIDE

<222> LOCATION: (1)..(819)

<223> OTHER INFORMATION: human Nig

<400> SEQUENCE: 7

Asp	Glu	Thr	Leu	Phe	Ala	Leu	Pro	Ala	Ala	Ser	Glu	Pro	Val	Ile	Arg
1				5					10					15	
Ser	Ser	Ala	Glu	Asn	Met	Asp	Leu	Lys	Glu	Gln	Pro	Gly	Asn	Thr	Ile
			20					25					30		
Ser	Ala	Gly	Gln	Glu	Asp	Phe	Pro	Ser	Val	Leu	Leu	Glu	Thr	Ala	Ala
		35					40					45			
Ser	Leu	Pro	Ser	Leu	Ser	Pro	Leu	Ser	Ala	Ala	Ser	Phe	Lys	Glu	His
	50					55					60				
Glu	Tyr	Leu	Gly	Asn	Leu	Ser	Thr	Val	Leu	Pro	Thr	Glu	Gly	Thr	Leu
65					70					75					80
Gln	Glu	Asn	Val	Ser	Glu	Ala	Ser	Lys	Glu	Val	Ser	Glu	Lys	Ala	Lys
				85					90					95	
Thr	Leu	Leu	Ile	Asp	Arg	Asp	Leu	Thr	Glu	Phe	Ser	Glu	Leu	Glu	Tyr
			100					105					110		
Ser	Glu	Met	Gly	Ser	Ser	Phe	Ser	Val	Ser	Pro	Lys	Ala	Glu	Ser	Ala
		115					120					125			
Val	Ile	Val	Ala	Asn	Pro	Arg	Glu	Glu	Ile	Ile	Val	Lys	Asn	Lys	Asp
	130					135					140				
Glu	Glu	Glu	Lys	Leu	Val	Ser	Asn	Asn	Ile	Leu	His	Asn	Gln	Gln	Glu
145				150						155					160
Leu	Pro	Thr	Ala	Leu	Thr	Lys	Leu	Val	Lys	Glu	Asp	Glu	Val	Val	Ser
				165					170					175	
Ser	Glu	Lys	Ala	Lys	Asp	Ser	Phe	Asn	Glu	Lys	Arg	Val	Ala	Val	Glu
			180					185					190		
Ala	Pro	Met	Arg	Glu	Glu	Tyr	Ala	Asp	Phe	Lys	Pro	Phe	Glu	Arg	Val
		195					200					205			
Trp	Glu	Val	Lys	Asp	Ser	Lys	Glu	Asp	Ser	Asp	Met	Leu	Ala	Ala	Gly
	210					215					220				
Gly	Lys	Ile	Glu	Ser	Asn	Leu	Glu	Ser	Lys	Val	Asp	Lys	Lys	Cys	Phe
225					230					235					240
Ala	Asp	Ser	Leu	Glu	Gln	Thr	Asn	His	Glu	Lys	Asp	Ser	Glu	Ser	Ser
			245						250					255	
Asn	Asp	Asp	Thr	Ser	Phe	Pro	Ser	Thr	Pro	Glu	Gly	Ile	Lys	Asp	Arg
			260					265					270		
Ser	Gly	Ala	Tyr	Ile	Thr	Cys	Ala	Pro	Phe	Asn	Pro	Ala	Ala	Thr	Glu
		275					280					285			
Ser	Ile	Ala	Thr	Asn	Ile	Phe	Pro	Leu	Leu	Gly	Asp	Pro	Thr	Ser	Glu
	290					295					300				
Asn	Lys	Thr	Asp	Glu	Lys	Lys	Ile	Glu	Glu	Lys	Lys	Ala	Gln	Ile	Val
305					310					315					320
Thr	Glu	Lys	Asn	Thr	Ser	Thr	Lys	Thr	Ser	Asn	Pro	Phe	Leu	Val	Ala
			325						330					335	
Ala	Gln	Asp	Ser	Glu	Thr	Asp	Tyr	Val	Thr	Thr	Asp	Asn	Leu	Thr	Lys
			340					345					350		
Val	Thr	Glu	Glu	Val	Val	Ala	Asn	Met	Pro	Glu	Gly	Leu	Thr	Pro	Asp
		355					360					365			
Leu	Val	Gln	Glu	Ala	Cys	Glu	Ser	Glu	Leu	Asn	Glu	Val	Thr	Gly	Thr
	370					375					380				
Lys	Ile	Ala	Tyr	Glu	Thr	Lys	Met	Asp	Leu	Val	Gln	Thr	Ser	Glu	Val
385					390					395					400
Met	Gln	Glu	Ser	Leu	Tyr	Pro	Ala	Ala	Gln	Leu	Cys	Pro	Ser	Phe	Glu
				405					410					415	
Glu	Ser	Glu	Ala	Thr	Pro	Ser	Pro	Val	Leu	Pro	Asp	Ile	Val	Met	Glu
			420					425					430		
Ala	Pro	Leu	Asn	Ser	Ala	Val	Pro	Ser	Ala	Gly	Ala	Ser	Val	Ile	Gln
		435					440					445			
Pro	Ser	Ser	Ser	Pro	Leu	Glu	Ala	Ser	Ser	Val	Asn	Tyr	Glu	Ser	Ile
	450					455					460				
Lys	His	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	Glu	Ala	Met	Ser	Val

465	Ser	Leu	Lys	Lys	Val	470	Ser	Gly	Ile	Lys	Glu	475	Glu	Ile	Lys	Glu	480	Pro	Glu
					485						490						495		
	Asn	Ile	Asn	Ala	Leu	Gln	Glu	Thr	505	Glu	Ala	Pro	Tyr	Ile	510	Ser	Ile		
	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	520	Lys	Leu	Ser	Ala	Glu	Pro	Ala	Pro		
			515											525					
	Asp	Phe	Ser	Asp	Tyr	Ser	Glu	Met	535	Ala	Lys	Val	Glu	Gln	Pro	Val	Pro		
		530											540						
	Asp	His	Ser	Glu	Leu	Val	Glu	Asp	Ser	Ser	Pro	Asp	Ser	Glu	Pro	Val			
		545				550					555						560		
	Asp	Leu	Phe	Ser	Asp	Asp	Ser	Ile	Pro	Asp	Val	Pro	Gln	Lys	Gln	Asp			
					565					570									
	Glu	Thr	Val	Met	Leu	Val	Lys	Glu	Ser	Leu	Thr	Glu	Thr	Ser	Phe	Glu			
				580					585					590					
	Ser	Met	Ile	Glu	Tyr	Glu	Asn	Lys	600	Glu	Lys	Leu	Ser	Ala	Leu	Pro	Pro		
			595											605					
	Glu	Gly	Gly	Lys	Pro	Tyr	Leu	Glu	Ser	Phe	Lys	Leu	Ser	Leu	Asp	Asn			
		610					615					620							
	Thr	Lys	Asp	Thr	Leu	Leu	Pro	Asp	Glu	Val	Ser	Thr	Leu	Ser	Lys	Lys			
		625				630					635					640			
	Glu	Lys	Ile	Pro	Leu	Gln	Met	Glu	Glu	Leu	Ser	Thr	Ala	Val	Tyr	Ser			
					645					650					655				
	Asn	Asp	Asp	Leu	Phe	Ile	Ser	Lys	Glu	Ala	Gln	Ile	Arg	Glu	Thr	Glu			
				660					665					670					
	Thr	Phe	Ser	Asp	Ser	Ser	Pro	Ile	Glu	Ile	Ile	Asp	Glu	Phe	Pro	Thr			
			675					680					685						
	Leu	Ile	Ser	Ser	Lys	Thr	Asp	Ser	Phe	Ser	Lys	Leu	Ala	Arg	Glu	Tyr			
		690					695					700							
	Thr	Asp	Leu	Glu	Val	Ser	His	Lys	Ser	Glu	Ile	Ala	Asn	Ala	Pro	Asp			
		705				710					715					720			
	Gly	Ala	Gly	Ser	Leu	Pro	Cys	Thr	Glu	Leu	Pro	His	Asp	Leu	Ser	Leu			
					725					730					735				
	Lys	Asn	Ile	Gln	Pro	Lys	Val	Glu	Glu	Lys	Ile	Ser	Phe	Ser	Asp	Asp			
				740					745					750					
	Phe	Ser	Lys	Asn	Gly	Ser	Ala	Thr	Ser	Lys	Val	Leu	Leu	Leu	Pro	Pro			
			755				760						765						
	Asp	Val	Ser	Ala	Leu	Ala	Thr	Gln	Ala	Glu	Ile	Glu	Ser	Ile	Val	Lys			
		770					775					780							
	Pro	Lys	Val	Leu	Val	Lys	Glu	Ala	Glu	Lys	Lys	Leu	Pro	Ser	Asp	Thr			
		785				790					795					800			
	Glu	Lys	Glu	Asp	Arg	Ser	Pro	Ser	Ala	Ile	Phe	Ser	Ala	Glu	Leu	Ser			
				805						810					815				
	Lys	Thr	Ser																

<210> SEQ ID NO 8
 <211> LENGTH: 10
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: BINDING
 <222> LOCATION: (1)..(10)
 <223> OTHER INFORMATION: hypervariable part of heavy chain of 11C7
 <400> SEQUENCE: 8
 Gly Phe Asp Phe Arg Arg Asn Trp Met Ser
 1 5 10

<210> SEQ ID NO 9
 <211> LENGTH: 17
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: BINDING
 <222> LOCATION: (1)..(17)
 <223> OTHER INFORMATION: hypervariable part of heavy chain of 11C7

<400> SEQUENCE: 9
 Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro Ser Leu Lys
 1 5 10 15
 Asp

<210> SEQ ID NO 10
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: BINDING
 <222> LOCATION: (1)..(9)
 <223> OTHER INFORMATION: hypervariable part of heavy chain of 11C7
 <400> SEQUENCE: 10
 Pro Val Trp Met Tyr Ala Met Asp Tyr
 1 5

<210> SEQ ID NO 11
 <211> LENGTH: 16
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: BINDING
 <222> LOCATION: (1)..(16)
 <223> OTHER INFORMATION: hypervariable part of light chain of 11C7
 <400> SEQUENCE: 11
 Lys Ser Ser Gln Ser Leu Leu His Ser Asp Gly Lys Thr Tyr Leu Asn
 1 5 10 15

<210> SEQ ID NO 12
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: BINDING
 <222> LOCATION: (1)..(7)
 <223> OTHER INFORMATION: hypervariable part of light chain of 11C7
 <400> SEQUENCE: 12
 Leu Val Ser Lys Leu Asp Ser
 1 5

<210> SEQ ID NO 13
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: BINDING
 <222> LOCATION: (1)..(9)
 <223> OTHER INFORMATION: hypervariable part of light chain of 11C7
 <400> SEQUENCE: 13
 Trp Gln Gly Thr His Phe Pro Gln Thr
 1 5

<210> SEQ ID NO 14
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: misc_binding
 <222> LOCATION: (1)..(30)
 <223> OTHER INFORMATION: DNA-CDR1-11C7
 <400> SEQUENCE: 14
 ggatttcgatt ttagaagaaa ttggatgagt

<210> SEQ ID NO 15
 <211> LENGTH: 51
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: misc_binding
 <222> LOCATION: (1)..(51)
 <223> OTHER INFORMATION: DNA-CDR2-11C7
 <400> SEQUENCE: 15
 gaaattaatc cagatagcag taagataaac tatacgccat ctctaaagga t 51

<210> SEQ ID NO 16
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: misc_binding
 <222> LOCATION: (1)..(27)
 <223> OTHER INFORMATION: DNA-CDR3-11C7
 <400> SEQUENCE: 16
 ccggtctgga tgtatgctat ggactac 27

<210> SEQ ID NO 17
 <211> LENGTH: 48
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: misc_binding
 <222> LOCATION: (1)..(48)
 <223> OTHER INFORMATION: DNA-CDR'1-11C7
 <400> SEQUENCE: 17
 aagtcaagtc agagcctctt gcatagtgat ggaaagacat atttgaat 48

<210> SEQ ID NO 18
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: misc_binding
 <222> LOCATION: (1)..(21)
 <223> OTHER INFORMATION: DNA-CDR'2-11C7
 <400> SEQUENCE: 18
 ctggtgtcta aactggactc t 21

<210> SEQ ID NO 19
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: misc_binding
 <222> LOCATION: (1)..(27)
 <223> OTHER INFORMATION: DNA-CDR'3-11C7
 <400> SEQUENCE: 19
 tggcaaggta cacattttcc tcagacg 27

<210> SEQ ID NO 20
 <211> LENGTH: 54
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:

<221> NAME/KEY: CDS
 <222> LOCATION: (1)..(54)
 <223> OTHER INFORMATION: leader sequence for heavy chain of 11C7
 <400> SEQUENCE: 20

atg gat ttt ggg ctg att ttt ttt att gtt ggt ctt tta aaa ggg gtc	48
Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val	
1 5 10 15	
cag tgt	54
Gln Cys	

<210> SEQ ID NO 21
 <211> LENGTH: 18
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <400> SEQUENCE: 21

Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
1 5 10 15
Gln Cys

<210> SEQ ID NO 22
 <211> LENGTH: 57
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(57)
 <223> OTHER INFORMATION: leader sequence for 11C7-light chain
 <400> SEQUENCE: 22

atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc tgg att cgg gaa	48
Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu	
1 5 10 15	
acc agc ggt	57
Thr Ser Gly	

<210> SEQ ID NO 23
 <211> LENGTH: 19
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <400> SEQUENCE: 23

Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
1 5 10 15
Thr Ser Gly

<210> SEQ ID NO 24
 <211> LENGTH: 181
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: PEPTIDE
 <222> LOCATION: (1)..(181)
 <223> OTHER INFORMATION: human Nig-D20
 <400> SEQUENCE: 24

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser	
1 5 10 15	
Glu Val Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser	
20 25 30	
Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val	
35 40 45	
Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val	
50 55 60	
Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu	

65	Ser	Ile	Lys	His	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	Glu	Ala	Met
	Ser	Val	Ser	Leu	85	Lys	Val	Ser	Gly	90	Ile	Lys	Glu	Glu	110	115
	Pro	Glu	Asn	Ile	100	Asn	Ala	Ala	Leu	105	Gln	Glu	Thr	Glu	Ala	Pro
	Ser	Ile	Ala	Cys	115	Asp	Leu	Ile	Lys	120	Glu	Thr	Lys	Leu	125	130
	Ala	Pro	Asp	Phe	130	Ser	Asp	Tyr	Ser	135	Glu	Met	Ala	Lys	Val	Glu
	Val	Pro	Asp	His	145	Ser	Glu	Leu	Val	150	Glu	Asp	Ser	Ser	Pro	Asp
	Pro	Val	Asp	Leu	165	Phe				170					175	
				180												

<210> SEQ ID NO 25
 <211> LENGTH: 3492
 <212> TYPE: DNA
 <213> ORGANISM: Rattus norvegicus
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(3492)
 <223> OTHER INFORMATION: rat NogoA
 <400> SEQUENCE: 25

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Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser Thr Asp Ser	
1 5 10 15	
ccg ccc cgg cct ccg ccc gcc ttc aag tac cag ttc gtg acg gag ccc	96
Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro	
20 25 30	
gag gac gag gag gac gag gag gag gag gag gac gag gag gag gac gac	144
Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp	
35 40 45	
gag gac cta gag gaa ctg gag gtg ctg gag agg aag ccc gca gcc ggg	192
Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly	
50 55 60	
ctg tcc gca gct gcg gtg ccg ccc gcc gcc gcc gcc gcg ccg ctg ctg gac	240
Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Pro Leu Leu Asp	
65 70 75 80	
ttc agc agc gac tcg gtg ccc ccc gcg ccc cgc ggg ccg ctg ccg gcc	288
Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala	
85 90 95	
gcg ccc cct gcc gct cct gag agg cag cca tcc tgg gaa cgc agc ccc	336
Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro	
100 105 110	
gcg gcg ccc gcg cca tcc ctg ccg ccc gct gcc gca gtc ctg ccc tcc	384
Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val Leu Pro Ser	
115 120 125	
aag ctc cca gag gac gac gag cct ccg gcg agg ccc ccg cct ccg ccg	432
Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro	
130 135 140	
cca gcc ggc gcg agc ccc ctg gcg gag ccc gcc gcg ccc cct tcc acg	480
Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr	
145 150 155 160	
ccg gcc gcg ccc aag cgc agg ggc tcc ggc tca gtg gat gag acc ctt	528
Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu	
165 170 175	
ttt gct ctt cct gct gca tct gag cct gtg ata ccc tcc tct gca gaa	576
Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu	
180 185 190	
aaa att atg gat ttg atg gag cag cca ggt aac act gtt tcg tct ggt	624
Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly	
195 200 205	
caa gag gat ttc cca tct gtc ctg ctt gaa act gct gcc tct ctt cct	672

Gln 210	Glu 210	Asp	Phe	Pro	Ser	Val 215	Leu	Leu	Glu	Thr	Ala 220	Ala	Ser	Leu	Pro	
tct Ser 225	cta Leu	tct Ser	cct Pro	ctc Leu	tca Ser 230	act Thr	gtt Val	tct Ser	ttt Phe 235	aaa Lys	gaa Glu	cat His	gga Gly	tac Tyr	ctt Leu 240	720
ggt Gly	aac Asn	tta Leu	tca Ser	gca Ala 245	gtg Val	tca Ser	tcc Ser	tca Ser	gaa Glu 250	gga Gly	aca Thr	att Ile	gaa Glu	gaa Glu 255	act Thr	768
tta Leu	aat Asn	gaa Glu	gct Ala 260	tct Ser	aaa Lys	gag Glu	ttg Leu	cca Pro 265	gag Glu	agg Arg	gca Ala	aca Thr	aat Asn 270	cca Pro	ttt Phe	816
gta Val	aat Asn	aga Arg 275	gat Asp	tta Leu	gca Ala	gaa Glu	ttt Phe 280	tca Ser	gaa Glu	tta Leu	gaa Glu	tat Tyr 285	tca Ser	gaa Glu	atg Met	864
gga Gly	tca Ser 290	tct Ser	ttt Phe	aaa Lys	ggc Gly	tcc Ser 295	cca Pro	aaa Lys	gga Gly	gag Glu	tca Ser 300	gcc Ala	ata Ile	tta Leu	gta Val	912
gaa Glu 305	aac Asn	act Thr	aag Lys	gaa Glu	gaa Glu 310	gta Val	att Ile	gtg Val	agg Arg	agt Ser 315	aaa Lys	gac Asp	aaa Lys	gag Glu	gat Asp 320	960
tta Leu	gtt Val	tgt Cys	agt Ser	gca Ala 325	gcc Ala	ctt Leu	cac His	agt Ser	cca Pro 330	caa Gln	gaa Glu	tca Ser	cct Pro	gtg Val 335	ggg Gly	1008
aaa Lys	gaa Glu	gac Asp	aga Arg 340	gtt Val	gtg Val	tct Ser	cca Pro	gaa Glu 345	aag Lys	aca Thr	atg Met	gac Asp 350	att Ile	ttt Phe	aat Asn	1056
gaa Glu	atg Met 355	cag Gln	atg Met	tca Ser	gta Val	gta Val	gca Ala 360	cct Pro	gtg Val	agg Arg	gaa Glu	gag Glu 365	tat Tyr	gca Ala	gac Asp	1104
ttt Phe 370	aag Lys	cca Pro	ttt Phe	gaa Glu	caa Gln	gca Ala 375	tgg Trp	gaa Glu	gtg Val	aaa Lys	gat Asp 380	act Thr	tat Tyr	gag Glu	gga Gly	1152
agt Ser 385	agg Arg	gat Asp	gtg Val	ctg Leu	gct Ala 390	gct Ala	aga Arg	gct Ala	aat Asn 395	gtg Val	gaa Glu	agt Ser	aaa Lys	gtg Val	gac Asp 400	1200
aga Arg	aaa Lys	tgc Cys	ttg Leu	gaa Glu 405	gat Asp	agc Ser	ctg Leu	gag Glu	caa Gln 410	aaa Lys	agt Ser	ctt Leu	ggg Gly 415	aag Lys	gat Asp	1248
agt Ser	gaa Glu	ggc Gly	aga Arg 420	aat Asn	gag Glu	gat Asp	gct Ala 425	tct Ser	ttc Phe	ccc Pro	agt Ser	acc Thr	cca Pro 430	gaa Glu	cct Pro	1296
gtg Val	aag Lys	gac Asp 435	agc Ser	tcc Ser	aga Arg	gca Ala	tat Tyr 440	att Ile	acc Thr	tgt Cys	gct Ala	tcc Ser 445	ttt Phe	acc Thr	tca Ser	1344
gca Ala 450	acc Thr	gaa Glu	agc Ser	acc Thr	aca Thr	gca Ala 455	act Asn	ttc Thr	cct Pro	ttg Leu 460	tta Leu	gaa Glu	gat Asp	cat His		1392
act Thr 465	tca Ser	gaa Glu	aat Asn	aaa Lys	aca Thr 470	gat Asp	gaa Glu	aaa Lys	aaa Lys	ata Ile 475	gaa Glu	gaa Glu	agg Arg	aag Lys	gcc Ala 480	1440
caa Gln	att Ile	ata Ile	aca Thr	gag Glu 485	aag Lys	act Thr	agc Ser	ccc Pro	aaa Lys 490	acg Thr	tca Ser	aat Asn	cct Pro	ttc Phe 495	ctt Leu	1488
gta Val	gca Ala	gta Val	cag Gln 500	gat Asp	tct Ser	gag Glu	gca Ala	gat Asp 505	tat Tyr	gtt Val	aca Thr	aca Thr	gat Asp 510	acc Thr	tta Leu	1536
tca Ser	aag Lys 515	gtg Val	act Thr	gag Glu	gca Ala	gca Ala	gtg Val 520	tca Ser	aac Asn	atg Met	cct Pro	gaa Glu 525	ggg Gly	ctg Leu	acg Thr	1584
cca Pro 530	gat Asp	tta Leu	gtt Val	cag Gln	gaa Glu	gca Ala 535	tgt Cys	gaa Glu	agt Ser	gaa Glu	ctg Leu 540	aat Asn	gaa Glu	gcc Ala	aca Thr	1632
ggg Gly 545	aca Thr	aag Lys	att Ile	gct Ala	tat Tyr 550	gaa Glu	aca Thr	aaa Lys	gtg Val	gac Asp 555	ttg Leu	gtc Val	caa Gln	aca Thr	tca Ser 560	1680

gaa Glu	gct Ala	ata Ile	caa Gln	gaa Glu 565	tca Ser	ctt Leu	tac Tyr	ccc Pro	aca Thr 570	gca Ala	cag Gln	ctt Leu	tgc Cys	cca Pro 575	tca Ser	1728
ttt Phe	gag Glu	gaa Glu	gct Ala 580	gaa Glu	gca Ala	act Thr	ccg Pro	tca Ser 585	cca Pro	gtt Val	ttg Leu	cct Pro	gat Asp 590	att Ile	gtt Val	1776
atg Met	gaa Glu	gca Ala 595	cca Pro	tta Leu	aat Asn	tct Ser	ctc Leu 600	ctt Leu	cca Pro	agc Ser	gct Ala	ggg Gly 605	gct Ala	tct Ser	gta Val	1824
gtg Val	cag Gln 610	ccc Pro	agt Ser	gta Val	tcc Ser	cca Pro 615	ctg Leu	gaa Glu	gca Ala	cct Pro	cct Pro 620	gaa Val	agt Ser	tat Tyr		1872
gac Asp 625	agt Ser	ata Ile	aag Lys	ctt Leu	gag Glu 630	cct Pro	gaa Glu	aac Asn	ccc Pro	cca Pro 635	cca Pro	tat Tyr	gaa Glu	gaa Glu	gcc Ala 640	1920
atg Met	aat Asn	gta Val	gca Ala	cta Leu 645	gct Lys	ttg Ala	gga Gly	aca Thr 650	aag Lys	gaa Glu	gga Gly	ata Ile	aaa Lys 655	gag Glu		1968
cct Pro	gaa Glu	agt Ser	ttt Phe 660	aat Asn	gca Ala	gct Ala	gtt Val	cag Gln 665	gaa Glu	aca Thr	gaa Glu	gct Ala	cct Pro 670	tat Tyr	ata Ile	2016
tcc Ser	att Ile	gag Ala 675	tgt Cys	gat Asp	tta Leu	att Ile	aaa Lys 680	aca Glu	aag Lys	ctc Leu	tcc Ser 685	act Thr	gag Glu	cca Pro		2064
agt Ser	cca Pro 690	gat Asp	ttc Phe	tct Ser	aat Asn	tat Tyr 695	tca Ser	gaa Glu	ata Ile	gca Ala	aaa Lys 700	ttc Phe	gag Glu	aag Lys	tcg Ser	2112
gtg Val 705	ccc Pro	gaa Glu	cac His	gct Ala 710	gag Glu	gtg Leu	gag Val	gat Glu	tcc Ser 715	cct Ser	cct Pro	gaa Glu	tct Ser	gaa Glu 720		2160
cca Pro	gtt Val	gac Asp	tta Leu	ttt Phe 725	agt Ser	gat Asp	gat Asp	tcg Ser	att Ile 730	cct Pro	gaa Glu	gtc Val	cca Pro	caa Gln 735	aca Thr	2208
caa Gln	gag Glu	gag Glu	gct Ala 740	gtg Val	atg Met	ctc Leu	atg Met	aag Lys 745	gag Glu	agt Ser	ctc Leu	act Thr	gaa Glu 750	gtg Val	tct Ser	2256
gag Glu	aca Thr	gta Val 755	gcc Ala	cag Gln	cac His	aaa Lys	gag Glu 760	gag Glu	aga Arg	ctt Leu	agt Ser	gcc Ala 765	tca Ser	cct Pro	cag Gln	2304
gag Glu	cta Leu 770	gga Gly	aag Lys	cca Pro	tat Tyr	tta Leu 775	gag Glu	tct Ser	ttt Phe	cag Gln	ccc Pro 780	aat Asn	tta Leu	cat His	agt Ser	2352
aca Thr 785	aaa Lys	gat Asp	gct Ala	gca Ala	tct Ser 790	aat Asn	gac Asp	att Ile	cca Pro	aca Thr 795	ttg Leu	acc Thr	aaa Lys	aag Lys	gag Glu 800	2400
aaa Lys	att Ile	tct Ser	ttg Leu	caa Gln 805	atg Met	gaa Glu	gag Glu	ttt Phe	aat Asn 810	act Thr	gca Ala	att Ile	tat Tyr	tca Ser 815	aat Asn	2448
gat Asp	gac Asp	tta Leu	ctt Leu 820	tct Ser	tct Ser	aag Lys	gaa Glu	gac Asp 825	aaa Lys	ata Ile	aaa Lys	gaa Glu	agt Ser 830	gaa Glu	aca Thr	2496
ttt Phe	tca Ser	gat Asp 835	tca Ser	tct Ser	ccg Pro	att Ile	gag Glu 840	ata Ile	gat Asp	gaa Glu	ttt Phe 845	ccc Pro	acg Thr	ttt Phe		2544
gtc Val	agt Ser 850	gct Ala	aaa Lys	gat Asp	gat Asp	tct Ser 855	cct Pro	aaa Lys	tta Leu	gcc Ala	aag Lys 860	gag Glu	tac Tyr	act Thr	gat Asp	2592
cta Leu 865	gaa Glu	gta Val	tcc Ser	gac Asp	aaa Lys 870	agt Ser	gaa Glu	att Ile	gct Ala	aat Asn 875	atc Ile	caa Gln	agc Ser	ggg Gly	gca Ala 880	2640
gat Asp	tca Ser	ttg Leu	cct Pro	tgc Cys 885	tta Leu	gaa Glu	ttg Leu	ccc Pro	tgt Cys 890	gac Asp	ctt Leu	tct Ser	ttc Phe	aag Lys 895	aat Asn	2688
ata Ile	tat Tyr	cct Pro	aaa Lys	gat Asp	gaa Glu	gta Val	cat His	gtt Val	tca Ser	gat Asp	gaa Glu	ttc Phe	tcc Ser	gaa Glu	aat Asn	2736

			900				905				910						
agg	tcc	agt	gta	tct	aag	gca	tcc	ata	tcg	cct	tca	aat	gtc	tct	gct		2784
Arg	Ser	Ser	Val	Ser	Lys	Ala	Ser	Ile	Ser	Pro	Ser	Asn	Val	Ser	Ala		
		915					920					925					
ttg	gaa	cct	cag	aca	gaa	atg	ggc	agc	ata	gtt	aaa	tcc	aaa	tca	ctt		2832
Leu	Glu	Pro	Gln	Thr	Glu	Met	Gly	Ser	Ile	Val	Lys	Ser	Lys	Ser	Leu		
	930					935					940						
acg	aaa	gaa	gca	gag	aaa	aaa	ctt	cct	tct	gac	aca	gag	aaa	gag	gac		2880
Thr	Lys	Glu	Ala	Glu	Lys	Lys	Leu	Pro	Ser	Asp	Thr	Glu	Lys	Glu	Asp		
945					950					955					960		
aga	tcc	ctg	tca	gct	gta	ttg	tca	gca	gag	ctg	agt	aaa	act	tca	gtt		2928
Arg	Ser	Leu	Ser	Ala	Val	Leu	Ser	Ala	Glu	Leu	Ser	Lys	Thr	Ser	Val		
				965					970					975			
gtt	gac	ctc	ctc	tac	tg	aga	gac	att	aag	aag	act	gga	gtg	gtg	ttt		2976
Val	Asp	Leu	Leu	Tyr	Trp	Arg	Asp	Ile	Lys	Lys	Thr	Gly	Val	Val	Phe		
		980						985					990				
ggt	gcc	agc	tta	ttc	ctg	ctg	ctg	tct	ctg	aca	gtg	ttc	agc	att	gtc		3024
Gly	Ala	Ser	Leu	Phe	Leu	Leu	Leu	Ser	Leu	Thr	Val	Phe	Ser	Ile	Val		
		995					1000					1005					
agt	gta	acg	gcc	tac	att	gcc	ttg	gcc	ctg	ctc	tcg	gtg	act	atc			3069
Ser	Val	Thr	Ala	Tyr	Ile	Ala	Leu	Ala	Leu	Leu	Ser	Val	Thr	Ile			
	1010					1015					1020						
agc	ttt	agg	ata	tat	aag	ggc	gtg	atc	cag	gct	atc	cag	aaa	tca			3114
Ser	Phe	Arg	Ile	Tyr	Lys	Gly	Val	Ile	Gln	Ala	Ile	Gln	Lys	Ser			
	1025					1030					1035						
gat	gaa	ggc	cac	cca	ttc	agg	gca	tat	tta	gaa	tct	gaa	gtt	gct			3159
Asp	Glu	Gly	His	Pro	Phe	Arg	Ala	Tyr	Leu	Glu	Ser	Glu	Val	Ala			
	1040					1045					1050						
ata	tca	gag	gaa	ttg	gtt	cag	aaa	tac	agt	aat	tct	gct	ctt	ggt			3204
Ile	Ser	Glu	Glu	Leu	Val	Gln	Lys	Tyr	Ser	Asn	Ser	Ala	Leu	Gly			
	1055					1060					1065						
cat	gtg	aac	agc	aca	ata	aaa	gaa	ctg	agg	cgg	ctt	ttc	tta	gtt			3249
His	Val	Asn	Ser	Thr	Ile	Lys	Glu	Leu	Arg	Arg	Leu	Phe	Leu	Val			
	1070					1075					1080						
gat	gat	tta	gtt	gat	tcc	ctg	aag	ttt	gca	gtg	ttg	atg	tg	gtg			3294
Asp	Asp	Leu	Val	Asp	Ser	Leu	Lys	Phe	Ala	Val	Leu	Met	Trp	Val			
	1085					1090					1095						
ttt	act	tat	gtt	ggt	gcc	ttg	ttc	aat	ggt	ctg	aca	cta	ctg	att			3339
Phe	Thr	Tyr	Val	Gly	Ala	Leu	Phe	Asn	Gly	Leu	Thr	Leu	Leu	Ile			
	1100					1105					1110						
tta	gct	ctg	atc	tca	ctc	ttc	agt	att	cct	gtt	att	tat	gaa	cgg			3384
Leu	Ala	Leu	Ile	Ser	Leu	Phe	Ser	Ile	Pro	Val	Ile	Tyr	Glu	Arg			
	1115					1120					1125						
cat	cag	gtg	cag	ata	gat	cat	tat	cta	gga	ctt	gca	aac	aag	agt			3429
His	Gln	Val	Gln	Ile	Asp	His	Tyr	Leu	Gly	Leu	Ala	Asn	Lys	Ser			
	1130					1135					1140						
gtt	aag	gat	gcc	atg	gcc	aaa	atc	caa	gca	aaa	atc	cct	gga	ttg			3474
Val	Lys	Asp	Ala	Met	Ala	Lys	Ile	Gln	Ala	Lys	Ile	Pro	Gly	Leu			
	1145					1150					1155						
aag	cgc	aaa	gca	gat	tga												3492
Lys	Arg	Lys	Ala	Asp													
	1160																

<210> SEQ ID NO 26

<211> LENGTH: 1163

<212> TYPE: PRT

<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 26

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Pro	Pro	Arg	Pro	Pro	Ala	Phe	Lys	Tyr	Gln	Phe	Val	Thr	Glu	Pro	
			20				25					30			
Glu	Asp	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Asp	Asp	
		35				40					45				

Glu	Asp	Leu	Glu	Glu	Leu	Glu	Val	Leu	Glu	Arg	Lys	Pro	Ala	Ala	Gly
Leu	50	Ser	Ala	Ala	Ala	Val	55	Pro	Pro	Ala	Ala	Ala	Pro	Leu	Asp
65		Ser	Ser	Asp	Ser	Val	70	Pro	Pro	Ala	75	Arg	Gly	Pro	Ala
				85						90				Leu	95
Ala	Pro	Pro	Ala	Ala	Pro	Glu	Arg	Gln	Pro	Ser	Trp	Glu	Arg	Ser	Pro
			100					105					110		
Ala	Ala	Pro	Ala	Pro	Ser	Leu	Pro	Pro	Ala	Ala	Ala	Val	125	Pro	Ser
			115					120							
Lys	Leu	Pro	Glu	Asp	Asp	Glu	Pro	Pro	Ala	Arg	Pro	Pro	Pro	Pro	Pro
	130					135					140				
Pro	Ala	Gly	Ala	Ser	Pro	Leu	Ala	Glu	Pro	Ala	Ala	Pro	Pro	Ser	Thr
145					150					155				160	
Pro	Ala	Ala	Pro	Lys	Arg	Arg	Gly	Ser	Gly	Ser	Val	Asp	Glu	Thr	Leu
				165					170					175	
Phe	Ala	Leu	Pro	Ala	Ala	Ser	Glu	Pro	Val	Ile	Pro	Ser	Ser	Ala	Glu
			180					185					190		
Lys	Ile	Met	Asp	Leu	Met	Glu	Gln	Pro	Gly	Asn	Thr	Val	Ser	Ser	Gly
		195					200					205			
Gln	Glu	Asp	Phe	Pro	Ser	Val	Leu	Leu	Glu	Thr	Ala	Ala	Ser	Leu	Pro
	210					215					220				
Ser	Leu	Ser	Pro	Leu	Ser	Thr	Val	Ser	Phe	Lys	Glu	His	Gly	Tyr	Leu
225					230					235				240	
Gly	Asn	Leu	Ser	Ala	Val	Ser	Ser	Ser	Glu	Gly	Thr	Ile	Glu	Glu	Thr
				245					250					255	
Leu	Asn	Glu	Ala	Ser	Lys	Glu	Leu	Pro	Glu	Arg	Ala	Thr	Asn	Pro	Phe
			260					265					270		
Val	Asn	Arg	Asp	Leu	Ala	Glu	Phe	Ser	Glu	Leu	Glu	Tyr	Ser	Glu	Met
		275					280					285			
Gly	Ser	Ser	Phe	Lys	Gly	Ser	Pro	Lys	Gly	Glu	Ser	Ala	Ile	Leu	Val
	290					295					300				
Glu	Asn	Thr	Lys	Glu	Glu	Val	Ile	Val	Arg	Ser	Lys	Asp	Lys	Glu	Asp
305					310					315				320	
Leu	Val	Cys	Ser	Ala	Ala	Leu	His	Ser	Pro	Gln	Glu	Ser	Pro	Val	Gly
				325					330					335	
Lys	Glu	Asp	Arg	Val	Val	Ser	Pro	Glu	Lys	Thr	Met	Asp	Ile	Phe	Asn
			340					345					350		
Glu	Met	Gln	Met	Ser	Val	Val	Ala	Pro	Val	Arg	Glu	Glu	Tyr	Ala	Asp
		355					360					365			
Phe	Lys	Pro	Phe	Glu	Gln	Ala	Trp	Glu	Val	Lys	Asp	Thr	Tyr	Glu	Gly
	370					375					380				
Ser	Arg	Asp	Val	Leu	Ala	Ala	Arg	Ala	Asn	Val	Glu	Ser	Lys	Val	Asp
385					390					395				400	
Arg	Lys	Cys	Leu	Glu	Asp	Ser	Leu	Glu	Gln	Lys	Ser	Leu	Gly	Lys	Asp
				405					410					415	
Ser	Glu	Gly	Arg	Asn	Glu	Asp	Ala	Ser	Phe	Pro	Ser	Thr	Pro	Glu	Pro
			420					425					430		
Val	Lys	Asp	Ser	Ser	Arg	Ala	Tyr	Ile	Thr	Cys	Ala	Ser	Phe	Thr	Ser
		435					440					445			
Ala	Thr	Glu	Ser	Thr	Thr	Ala	Asn	Thr	Phe	Pro	Leu	Glu	Glu	Asp	His
	450					455					460				
Thr	Ser	Glu	Asn	Lys	Thr	Asp	Glu	Lys	Lys	Ile	Glu	Glu	Arg	Lys	Ala
465					470					475				480	
Gln	Ile	Ile	Thr	Glu	Lys	Thr	Ser	Pro	Lys	Thr	Ser	Asn	Pro	Phe	Leu
				485					490					495	
Val	Ala	Val	Gln	Asp	Ser	Glu	Ala	Asp	Tyr	Val	Thr	Thr	Asp	Thr	Leu
			500					505					510		
Ser	Lys	Val	Thr	Glu	Ala	Ala	Val	Ser	Asn	Met	Pro	Glu	Gly	Leu	Thr
		515					520					525			
Pro	Asp	Leu	Val	Gln	Glu	Ala	Cys	Glu	Ser	Glu	Leu	Asn	Glu	Ala	Thr
	530					535					540				
Gly	Thr	Lys	Ile	Ala	Tyr	Glu	Thr	Lys	Val	Asp	Leu	Val	Gln	Thr	Ser
545					550					555				560	
Glu	Ala	Ile	Gln	Glu	Ser	Leu	Tyr	Pro	Thr	Ala	Gln	Leu	Cys	Pro	Ser

Phe	Glu	Glu	Ala	565 Glu	Ala	Thr	Pro	Ser	570 Pro	Val	Leu	Pro	Asp	575 Ile	Val
Met	Glu	Ala	580 Pro	Leu	Asn	Ser	Leu	585 Leu	Pro	Ser	Ala	Gly	590 Ala	Ser	Val
Val	Gln	Pro	Ser	Val	Ser	Pro	Leu	Glu	Ala	Pro	Pro	Pro	Val	Ser	Tyr
Asp	Ser	Ile	Lys	Leu	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	Glu	Ala
Met	Asn	Val	Ala	Leu	Lys	Ala	Leu	Gly	Thr	Lys	Glu	Gly	Ile	Lys	Glu
Pro	Glu	Ser	Phe	Asn	Ala	Ala	Val	Gln	Glu	Thr	Glu	Ala	Pro	Tyr	Ile
Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu	Ser	Thr	Glu	Pro
Ser	Pro	Asp	Phe	Ser	Asn	Tyr	Ser	Glu	Ile	Ala	Lys	Phe	Glu	Lys	Ser
Val	Pro	Glu	His	Ala	Glu	Leu	Val	Glu	Asp	Ser	Ser	Pro	Glu	Ser	Glu
Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp	Ser	Ile	Pro	Glu	Val	Pro	Gln	Thr
Gln	Glu	Glu	Ala	Val	Met	Leu	Met	Lys	Glu	Ser	Leu	Thr	Glu	Val	Ser
Glu	Thr	Val	Ala	Gln	His	Lys	Glu	Glu	Arg	Leu	Ser	Ala	Ser	Pro	Gln
Glu	Leu	Gly	Lys	Pro	Tyr	Leu	Glu	Ser	Phe	Gln	Pro	Asn	Leu	His	Ser
Thr	Lys	Asp	Ala	Ala	Ser	Asn	Asp	Ile	Pro	Thr	Leu	Thr	Lys	Lys	Glu
Lys	Ile	Ser	Leu	Gln	Met	Glu	Glu	Phe	Asn	Thr	Ala	Ile	Tyr	Ser	Asn
Asp	Asp	Leu	Leu	Ser	Ser	Lys	Glu	Asp	Lys	Ile	Lys	Glu	Ser	Glu	Thr
Phe	Ser	Asp	Ser	Ser	Pro	Ile	Glu	Ile	Ile	Asp	Glu	Phe	Pro	Thr	Phe
Val	Ser	Ala	Lys	Asp	Asp	Ser	Pro	Lys	Leu	Ala	Lys	Glu	Tyr	Thr	Asp
Leu	Glu	Val	Ser	Asp	Lys	Ser	Glu	Ile	Ala	Asn	Ile	Gln	Ser	Gly	Ala
Asp	Ser	Leu	Pro	Cys	Leu	Glu	Leu	Pro	Cys	Asp	Leu	Ser	Phe	Lys	Asn
Ile	Tyr	Pro	Lys	Asp	Glu	Val	His	Val	Ser	Asp	Glu	Phe	Ser	Glu	Asn
Arg	Ser	Ser	Val	Ser	Lys	Ala	Ser	Ile	Ser	Pro	Ser	Asn	Val	Ser	Ala
Leu	Glu	Pro	Gln	Thr	Glu	Met	Gly	Ser	Ile	Val	Lys	Ser	Lys	Ser	Leu
Thr	Lys	Glu	Ala	Glu	Lys	Lys	Leu	Pro	Ser	Asp	Thr	Glu	Lys	Glu	Asp
Arg	Ser	Leu	Ser	Ala	Val	Leu	Ser	Ala	Glu	Leu	Ser	Lys	Thr	Ser	Val
Val	Asp	Leu	Leu	Tyr	Trp	Arg	Asp	Ile	Lys	Lys	Thr	Gly	Val	Val	Phe
Gly	Ala	Ser	Leu	Phe	Leu	Leu	Leu	Ser	Leu	Thr	Val	Phe	Ser	Ile	Val
Ser	Val	Thr	Ala	Tyr	Ile	Ala	Leu	Ala	Leu	Leu	Ser	Val	Thr	Ile	
Ser	Phe	Arg	Ile	Tyr	Lys	Gly	Val	Ile	Gln	Ala	Ile	Gln	Lys	Ser	
Asp	Glu	Gly	His	Pro	Phe	Arg	Ala	Tyr	Leu	Glu	Ser	Glu	Val	Ala	
Ile	Ser	Glu	Glu	Leu	Val	Gln	Lys	Tyr	Ser	Asn	Ser	Ala	Leu	Gly	
His	Val	Asn	Ser	Thr	Ile	Lys	Glu	Leu	Arg	Arg	Leu	Phe	Leu	Val	

Asp	Asp	Leu	Val	Asp	Ser	Leu	Lys	Phe	Ala	Val	Leu	Met	Trp	Val
1085						1090					1095			
Phe	Thr	Tyr	Val	Gly	Ala	Leu	Phe	Asn	Gly	Leu	Thr	Leu	Leu	Ile
1100						1105					1110			
Leu	Ala	Leu	Ile	Ser	Leu	Phe	Ser	Ile	Pro	Val	Ile	Tyr	Glu	Arg
1115						1120					1125			
His	Gln	Val	Gln	Ile	Asp	His	Tyr	Leu	Gly	Leu	Ala	Asn	Lys	Ser
1130						1135					1140			
Val	Lys	Asp	Ala	Met	Ala	Lys	Ile	Gln	Ala	Lys	Ile	Pro	Gly	Leu
1145						1150					1155			
Lys	Arg	Lys	Ala	Asp										
1160														

<210> SEQ ID NO 27
 <211> LENGTH: 25
 <212> TYPE: PRT
 <213> ORGANISM: Rattus norvegicus
 <220> FEATURE:
 <221> NAME/KEY: PEPTIDE
 <222> LOCATION: (1)..(25)
 <223> OTHER INFORMATION: rat PEP4
 <400> SEQUENCE: 27
 Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn
 1 5 10 15
 Ser Thr Ile Lys Glu Leu Arg Arg Leu
 20 25

<210> SEQ ID NO 28
 <211> LENGTH: 17
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: PRO/SER rich peptide
 <220> FEATURE:
 <221> NAME/KEY: PEPTIDE
 <222> LOCATION: (1)..(17)
 <223> OTHER INFORMATION: Synthetic peptide
 <400> SEQUENCE: 28
 Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro
 1 5 10 15
 Ser

<210> SEQ ID NO 29
 <211> LENGTH: 25
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: CA-NA-2F
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(25)
 <223> OTHER INFORMATION: CA-NA-2F primer
 <400> SEQUENCE: 29
 aagcaccatt gaattctgca gttcc

25

<210> SEQ ID NO 30
 <211> LENGTH: 28
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:

<223> OTHER INFORMATION: CA-NA-3R
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(28)
 <223> OTHER INFORMATION:
 <400> SEQUENCE: 30
 aactgcagta ctgagctcct ccatctgc

28

<210> SEQ ID NO 31
 <211> LENGTH: 33
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: forward 5'
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(33)
 <223> OTHER INFORMATION: forward primer
 <400> SEQUENCE: 31
 gtcgcggatc catggagacc ctttttgctc ttc

33

<210> SEQ ID NO 32
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: reverse 5'
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(27)
 <223> OTHER INFORMATION: reverse primer
 <400> SEQUENCE: 32
 gttctcgagt tatgaagttt tactcag

27

<210> SEQ ID NO 33
 <211> LENGTH: 29
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: forward 5'-1
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(29)
 <223> OTHER INFORMATION: primer
 <400> SEQUENCE: 33
 gtgcggatcc atggatttga aggagcagc

29

<210> SEQ ID NO 34
 <211> LENGTH: 28
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: reverse 5'-1
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(28)
 <223> OTHER INFORMATION: primer
 <400> SEQUENCE: 34
 gtttctcgag tgaagtttta ttcagctc

28

<210> SEQ ID NO 35

<211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: 5' primer
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(20)
 <223> OTHER INFORMATION: primer
 <400> SEQUENCE: 35
 tccaccccg ccgcgccaa

20

<210> SEQ ID NO 36
 <211> LENGTH: 22
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: 5' primer 2
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(22)
 <223> OTHER INFORMATION: primer
 <400> SEQUENCE: 36
 aatgatgggc aaagctgtgc tg

22

<210> SEQ ID NO 37
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: 3' primer
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(24)
 <223> OTHER INFORMATION: primer
 <400> SEQUENCE: 37
 ggtacaaaga ttgcttatga aaca

24

<210> SEQ ID NO 38
 <211> LENGTH: 22
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: 3' primer 2
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(22)
 <223> OTHER INFORMATION: primer
 <400> SEQUENCE: 38
 agcagggcca aggcaatgta gg

22

<210> SEQ ID NO 39
 <211> LENGTH: 28
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: 5'-VL leader
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(28)

<223> OTHER INFORMATION: primer
 <400> SEQUENCE: 39
 aatatgagtc ctgcccagtt cctgtttc 28

<210> SEQ ID NO 40
 <211> LENGTH: 32
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: 3'-Ck
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(32)
 <223> OTHER INFORMATION: primer
 <400> SEQUENCE: 40
 ttaggaattc ctaacactct cccctgttga ag 32

<210> SEQ ID NO 41
 <211> LENGTH: 31
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: 5'-VH leader
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(31)
 <223> OTHER INFORMATION: primer
 <400> SEQUENCE: 41
 aatatggatt ttgggctgat tttttttatt g 31

<210> SEQ ID NO 42
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: 3'-CH hinge
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(24)
 <223> OTHER INFORMATION: primer
 <400> SEQUENCE: 42
 aattgggcaa cgttgcaggt gacg 24

<210> SEQ ID NO 43
 <211> LENGTH: 663
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: misc_binding
 <222> LOCATION: (1)..(663)
 <223> OTHER INFORMATION: DNA variable part of heavy chain 11C7
 <400> SEQUENCE: 43

atggattttg	ggctgatttt	ttttattggt	ggctttttta	aaggggtcca	gtgtgaggtg	60
aagctttctg	agctctggag	tggcctgggt	cagcctggag	gatccctgaa	actctcctgt	120
gtagtctcag	gattcgaatt	tagaagaaat	tggatgagtt	gggtccggca	ggctcctggg	180
aaagggctag	aatggattgg	agaaattaat	ccagatagca	gtaagataaa	ctatacgcca	240
tctctaaagg	ataaattcat	catctccaga	gacaatgcca	agaatacgct	gtacctgcaa	300
gtgagcacag	tgagatctga	ggacacagcc	ctttattact	gtgtgagacc	ggctctggatg	360
tatgctatgg	actactgggg	tcaaggaacc	tcagtcaccg	tctcctcagc	caaaacgaca	420
cccccatctg	tctatccact	ggccccctga	tctgctgccc	aaactaactc	catggtgacc	480
ctgggatgcc	tggtcaaggg	ctatttcctt	gagccagtga	cagtgacctg	gaactctgga	540

tccctgtcca	gcggtgtgca	caccttccca	gctgtcctgc	agtctgacct	ctacactctg	600
agcagctcag	tgactgtccc	ctccagcacc	tggcccagcg	agaccgtcac	ctgcaacgtt	660
gcc						663

<210> SEQ ID NO 44
 <211> LENGTH: 717
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: misc_binding
 <222> LOCATION: (1)..(717)
 <223> OTHER INFORMATION: variable part of light chain of 11C7
 <400> SEQUENCE: 44

atgagtcctg	cccagttcct	gtttctgtta	gtgctctgga	ttcgggaaac	cagcggtgat	60
gttctgttga	cccagactcc	tctcactttg	tcgataacca	ttggacaacc	agcctccatc	120
tcttgcaagt	caagtcagag	cctcttgcac	agtgatggaa	agacatattt	gaattgggtg	180
ttacagaggc	caggccagtc	tccaaagcgc	ctaactctatc	tggtgtctaa	actggactct	240
ggagtccttg	acaggttcac	tggcagtgga	tcagggacgg	atttcacact	gaaaatcagc	300
agagtgaggg	ctgaggattt	gggactttat	tattgctggc	aaggtaacac	ttttcctcag	360
acgttcgggtg	gaggcaccaa	gctggaaatc	aaacgggctg	atgctgcacc	aactgtatcc	420
atcttcccac	catccagtgga	gcagttaaca	tctggaggtg	cctcagtcgt	gtgcttcttg	480
aacaacttct	accccaaaga	catcaatgtc	aagtgggaaga	ttgatggcag	tgaacgacaa	540
aatggcgctc	tgaacagttg	gactgatcag	gacagcaaag	acagcaccta	cagcatgagc	600
agcaccctca	cgttgaccaa	ggacgagtat	gaacgacata	acagctatac	ctgtgaggcc	660
actcacaaga	catcaacttc	acccattgtc	aagagcttca	acaggggaga	gtgttag	717

<210> SEQ ID NO 45
 <211> LENGTH: 239
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 45

Thr	Lys	Val	Thr	Glu	Val	Val	Ala	Asn	Met	Pro	Glu	Gly	Leu	Thr
1			5					10				15		
Pro	Asp	Leu	Val	Gln	Glu	Ala	Cys	Glu	Ser	Glu	Leu	Asn	Glu	Val
		20						25				30		
Gly	Thr	Lys	Ile	Ala	Tyr	Glu	Thr	Lys	Met	Asp	Leu	Val	Gln	Thr
		35					40				45			
Glu	Val	Met	Gln	Glu	Ser	Leu	Tyr	Pro	Ala	Ala	Gln	Leu	Cys	Pro
	50					55				60				
Phe	Glu	Glu	Ser	Glu	Ala	Thr	Pro	Ser	Pro	Val	Leu	Pro	Asp	Ile
65				70				75						80
Met	Glu	Ala	Pro	Leu	Asn	Ser	Ala	Val	Pro	Ser	Ala	Gly	Ala	Ser
			85				90					95		
Ile	Gln	Pro	Ser	Ser	Pro	Leu	Glu	Ala	Ser	Ser	Val	Asn	Tyr	Glu
		100					105					110		
Ser	Ile	Lys	His	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	Glu	Ala
	115						120				125			
Ser	Val	Ser	Leu	Lys	Lys	Val	Ser	Gly	Ile	Lys	Glu	Glu	Ile	Lys
	130					135				140				
Pro	Glu	Asn	Ile	Asn	Ala	Ala	Leu	Gln	Glu	Thr	Glu	Ala	Pro	Tyr
	145			150				155						160
Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu	Ser	Ala	Glu
			165					170					175	
Ala	Pro	Asp	Phe	Ser	Asp	Tyr	Ser	Glu	Met	Ala	Lys	Val	Glu	Gln
		180					185					190		
Val	Pro	Asp	His	Ser	Glu	Leu	Val	Glu	Asp	Ser	Ser	Pro	Asp	Ser
	195						200					205		
Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp	Ser	Ile	Pro	Asp	Val	Pro	Gln
	210					215					220			

Gln Asp Glu Thr Val Met Leu Val Lys Glu Ser Leu Thr Glu Thr
 225 230 235

<210> SEQ ID NO 46

<211> LENGTH: 239

<212> TYPE: PRT

<213> ORGANISM: Pan paniscus

<400> SEQUENCE: 46

Gly Lys Val Thr Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr
 1 5 10 15
 Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr
 20 25 30
 Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser
 35 40 45
 Glu Val Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser
 50 55 60
 Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
 65 70 75 80
 Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Ala
 85 90 95
 Val Gln Pro Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu
 100 105 110
 Ser Ile Ile His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met
 115 120 125
 Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu
 130 135 140
 Pro Glu Ser Ile Asn Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
 145 150 155 160
 Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro
 165 170 175
 Thr Pro Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro
 180 185 190
 Val Pro Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu
 195 200 205
 Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys
 210 215 220
 Gln Asp Glu Ala Val Met Leu Val Lys Glu Asn Leu Pro Glu Thr
 225 230 235

<210> SEQ ID NO 47

<211> LENGTH: 239

<212> TYPE: PRT

<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 47

Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr
 1 5 10 15
 Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr
 20 25 30
 Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser
 35 40 45
 Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser
 50 55 60
 Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
 65 70 75 80
 Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val
 85 90 95
 Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
 100 105 110
 Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
 115 120 125
 Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu
 130 135 140
 Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile

145	Ser	Ile	Ala	Cys	Asp	150	Leu	Ile	Lys	Glu	Thr	155	Lys	Leu	Ser	Thr	Glu	160	Pro
	Ser	Pro	Asp	Phe	165	Asn	Tyr	Ser	Glu	170	Ile	Ala	Lys	Phe	Glu	175	Lys	Ser	
	Val	Pro	Glu	His	180	Ala	Glu	Leu	Val	185	Glu	Asp	Ser	Ser	Pro	Glu	Ser	Glu	
	Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp	Ser	200	Ile	Pro	Glu	Val	Pro	Gln	Thr		
	Gln	Glu	Glu	Ala	Val	Met	215	Leu	Met	Lys	Glu	Ser	220	Leu	Thr	Glu	Val		
225						230						235							

<210> SEQ ID NO 48

<211> LENGTH: 239

<212> TYPE: PRT

<213> Mus musculus

<400> SEQUENCE: 48

Ser	Lys	Val	Thr	Glu	Ala	Val	Val	Ala	Thr	Met	Pro	Glu	Gly	Leu	Thr
1				5					10					15	
Pro	Asp	Leu	Val	Gln	Glu	Ala	Cys	Glu	Ser	Glu	Leu	Asn	Glu	Ala	Thr
			20					25					30		
Gly	Thr	Lys	Ile	Ala	Tyr	Glu	Thr	Lys	Val	Asp	Leu	Val	Gln	Thr	Ser
		35					40					45			
Glu	Ala	Ile	Gln	Glu	Ser	Ile	Tyr	Pro	Thr	Ala	Gln	Leu	Cys	Pro	Ser
	50					55				60					
Phe	Glu	Glu	Ala	Glu	Ala	Thr	Pro	Ser	Pro	Val	Leu	Pro	Asp	Ile	Val
65					70					75				80	
Met	Glu	Ala	Pro	Leu	Asn	Ser	Leu	Leu	Pro	Ser	Thr	Gly	Ala	Ser	Val
			85						90					95	
Ala	Gln	Pro	Ser	Ala	Ser	Pro	Leu	Glu	Val	Pro	Ser	Pro	Val	Ser	Tyr
			100					105					110		
Asp	Gly	Ile	Lys	Leu	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	Glu	Ala
		115					120					125			
Met	Ser	Val	Ala	Leu	Lys	Thr	Ser	Asp	Ser	Lys	Glu	Glu	Ile	Lys	Glu
	130					135					140				
Pro	Glu	Ser	Phe	Asn	Ala	Ala	Ala	Gln	Glu	Ala	Glu	Ala	Pro	Tyr	Ile
145				150						155				160	
Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu	Ser	Thr	Glu	Pro
			165						170					175	
Ser	Pro	Glu	Phe	Ser	Asn	Tyr	Ser	Glu	Ile	Ala	Lys	Phe	Glu	Lys	Ser
			180					185					190		
Val	Pro	Asp	His	Cys	Glu	Leu	Val	Asp	Asp	Ser	Ser	Pro	Glu	Ser	Glu
		195					200					205			
Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp	Ser	Ile	Pro	Glu	Val	Pro	Gln	Thr
	210					215					220				
Gln	Glu	Glu	Ala	Val	Met	Leu	Met	Lys	Glu	Ser	Leu	Thr	Glu	Val	
225					230					235					